

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:39:13 ; Search time 1839.23 Seconds
(without alignments)
16145.302 Million cell updates/sec

Title: US-09-645-337-3

Perfect score: 1800

Sequence: 1 gtgccacacactctagtaa.....acgcgtgcatgagacgtcat 1800

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pi:*
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10: gb_ro:*
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34: em_htg_inv:*
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36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1799	99.9	1800	6	AX139016	AX139016 Sequence
2	1732	96.2	1733	8	AF195548	AF195548 Arabidops
3	712.8	39.6	81662	8	AB008265	AB008265 Arabidops
4	615.6	34.2	1742	8	AF045473	AF045473 Zea mays
5	549.6	30.5	1906	8	AF384032	AF384032 Zea mays
6	525.2	29.2	2047	8	AF035815	AF035815 Zea mays
7	523.4	29.1	1807	6	AX139014	AX139014 Sequence
8	523.4	29.1	1807	8	AF195547	AF195547 Arabidops
9	523.4	29.1	1808	8	AF014824	AF014824 Arabidops
10	503.8	28.0	1579	8	AF332875	AF332875 Oryza sat
11	496.2	27.6	1839	8	AF282858	AF282858 Mesembrya
12	462	25.7	2172	3	DMHLSSEAC	Y09258 D.melanogas
13	459.2	25.5	1878	5	AF039752	AF039752 Gallus ga
14	458.6	25.5	2073	3	AF026949	AF026949 Drosophil
15	444.6	24.7	1985	6	AX053103	AX053103 Sequence
16	444.6	24.7	1985	9	HSU31814	U31814 Human trans
17	441.8	24.5	1997	10	MMU31758	U31758 Mus musculu
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27	433	24.1	1999	10	MMU80780	U80780 Mus musculu
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39	403.6	22.4	8223	8	SCDNANO	X83226 S.cerevisia
40	403	22.4	2544	8	AY035205	AY035205 Kluyverom
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42	379.8	21.1	1920	9	AF039703	AF039703 Homo sapi
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45	378.6	21.0	1975	10	AF074881	AF074881 Mus muscu

ALIGNMENTS

RESULT 1

AX139016

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

PAT 30-MAY-2001

AX139016 1800 bp DNA

Sequence 3 from Patent EP1094112.

AX139016

AX139016.1 GI:14274699

thale cress.

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 1800)

Wu,K., Miki,B.L., Tian,L. and Brown,D.C.

Repressing gene expression in plants

Patent: EP 1094112-A 3 25-APR-2001;

The Minister of Agriculture and Agri-Food (CA)

Location/Qualifiers

1. 1800

/organism="Arabidopsis thaliana"

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 VERSION AF195548.1 GI:11066140
 KEYWORDS thale cress.
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1733)
 REFERENCE Wu, K., Malik, K., Tian, L., Brown, D. and Miki, B.
 AUTHORS Functional analysis of RPD3 histone deacetylase homologs in

JOURNAL Arabidopsis thaliana
 REFERENCE 2 (bases 1 to 1733)
 AUTHORS Wu, K., Tian, L., Malik, K., Brown, D. and Miki, B.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1999) Eastern Cereal and Oilseed Research Centre,
 Agriculture and Agri-Food Canada, Ottawa, Ontario K1A 0C6, Canada
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 /cultivar="Columbia"
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BASE COUNT 453 a 374 c 439 g 466 t 1 others
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 Best Local Similarity 100.0%; Pred. No. 0;
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AB008265.1 GI:2618600
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AB008265.1 GI:2618600
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clone:MDC12.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (sites)
Nakamura,Y., Sato,S., Kaneko,T., Kotani,H., Asamizu,E., Miyajima,N.
and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. III.
Seventeen physically assigned P1 clones
DNA Res. 4 (6), 401-414 (1997)
98162728
2 (bases 1 to 81662)
Nakamura,Y.
Direct Submission
Submitted (24-OCT-1997) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research, 1532-3, Yana
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd-graph.cgi?c=MDC12
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlin.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is M822 and the 3' clone is K921.
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Query Match 39.6%; Score 712.8; DB 8; Length 81662;

Best Local Similarity 70.8%; Pred. No. 5.4e-190;

Matches 1245; Conservative 0; Mismatches 2; Indels 511; Gaps 2;

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QY 121 atgagggcagacgaaagcggcatctctcgcgctgggagcccgagcgtaaagcgga 180
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QY 181 gtcagttacttctacgagccacacatcgagactactactacgtccaagccacccccgag 240
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Db 26802 GTCAGTTACTTCTACGAGCCGACGATCGAGACTACTACTAGGTCAGGCCACCCGATG 26743
QY 241 aagctcaccggatccgtatggctcatagcctaatactcaactcaccctccgctgc 300
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Db 26742 AAGCTCACCGGATCGGTATGGCTCATAGCTAATCAATCACTATCACTCCACCGTGGC 26683
QY 301 ttagaatcagtcgacctagctcgctgacgcctccgatatcgccgagttccattcgccg 360
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Db 26682 TTAGAAATCAGTGGCCCTAGGCTCGCTGACGCTCCGATATCGGCGGATTCATTCGCGC 26623
QY 361 gagtattgacttctcctcgtcttcggttcggaatctatggcgatctcttcgctgca 420
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QY 421 cgaacctaaagcgattcaatgctggtgagattgctctgcttcgacggacttttgaat 480
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QY 659 ----- 658
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QY	844	gatggttatggcagatgaagtttccgcagcttgtttagacctctatccaaaagttatg	903	
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QY	964	cggttgggttgcctcaacctatcagtcacaaaggttcaacgttgattgcttcggtctttaa	1023	
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QY	1084	cgttactgagttatg-----	1099	
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Db	25302	CCCAGATTATACGCTTCATGTGCACCCAGTCCCTATGGAGAAATTTAAACACGCCCAAGA	25243	
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RESULTS

RESULTS	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	PLN	28-JAN-1999
AF045473	1742 bp	zebra mays histone deacetylase (hdhb)	AF045473	GI:4193319	zebra mays.	zebra mays	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.	PLN	28-JAN-1999

REFERENCE

REFERENCE
AUTHORS

AUTHORS	TITLE
W. J. G. B. van den Broek, J. A. M. M. van't Hof-Grootenboer, and J. A. M. M. van't Hof-Grootenboer	...

TITLE
 TOPICAL

JOURNAL

SECRET

FEATURES

source

gene

CDS

—

—

3' UTR	1378..1742	/gene="h1b"	407 a	457 c	453 g	425 t
BASE COUNT						

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Qy	917	cagaggcagttgttcttcagtgtagtgtagtgcactccttaagtggatcggttgaggttgc 976
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Qy	977	tcaacttatcagtcacaaggttcacgtcctgaatgccttcggttccttaagatccttacaacgttc 1036
Db	987	TCAATCTTCAATCAAGGTCATGCTGAGTGGCGTCAAAATTTATGAGATCGTTCATGTTTC 1046
Qy	1037	ctctcatggtgttggttggtgaaggtatactattctgaataatgttgcctgttcgttggttt 1096
Db	1047	CCCTACTGCTCTTGGTGGTGGTGTGTACACTATCCGCAATGTTGCCGTTGCTGGTGCT 1106
Qy	1097	atgagatgcagttgctgtgtgagtagagccggacacaaactccttacaatgagttatt 1156
Db	1107	ACGAGACTGGAGTGTGCATCTTGAGTGTGAAGTGAAGACCAAGATCCGGAGCATGAATATT 1166
Qy	1157	ttgagttatcgcgccagattatcagctttcttcattcgcacccaagtcctatgagaaatttaa 1216
Db	1167	ATGAATACTTTGGTCCAGACTTATACATTTCAAGTGTCTCAAGTAAACATGAGAAATAAGA 1226
Qy	1217	acagcccaagatatggagaggaataagacacagcttgtcggaacacatttcggagactaa 1276
Db	1227	ATTCTGTCAGATGCTTGAAGAGATTGCAATGACCTTCTCCACAATCTCTTAAGCTTC 1286
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AF332875	1579 bp	mrna PLN 07-FEB-2001
LOCUS	Oryza sativa histone deacetylase HD1 mRNA, complete cds.	
DEFINITION	Oryza sativa histone deacetylase HD1 mRNA, complete cds.	
ACCESSION	AF332875	
VERSION	AF332875.1	GI:12698879
KEYWORDS		
SOURCE	Oryza sativa.	
ORGANISM	Oryza sativa	
REFERENCE	1 (bases 1 to 1579)	
AUTHORS	Song,F. and Goodman,R.M.	
TITLE	Molecular characterization of a rice histone deacetylase gene OsHD1	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1579)	
AUTHORS	Song,F. and Goodman,R.M.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-DEC-2000) Department of Plant Pathology, University of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 5706, USA	
FEATURES	Location/Qualifiers	
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CDS		

ORIGIN

Query Match 25.7%; Score 462; DB 3; Length 2172;
Best Local Similarity 64.3%; Pred. No. 2.5e-119;
Matches 728; Conservative 0; Mismatches 395; Indels 9; Gaps 2;

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QY 350 tccattgcgcgagatgacttctcctcctcctcctcctcctcctcctcctcctcctc 409
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DB 648 CGGAAGCCTCGGCTTCGCTACGTCAATGATGTTCTGCGGAATCTGGAACCTGCTTA 707

QY 650 agatgtttaagcgggttctacatagatatgtatgctccacatggagatgagtgaaag 709
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QY 710 aagcgttttacaccactagatgactgacttcttcttccacaaatttgggagctttt 769
DB 768 AGCGGCTTATACCAACCGATCGTGTGATGACTGTGACGCTTCCCAAGTACGAGATAT 827

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DB 1068 TGGAGTTCGTGAAGAAATATAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127

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RESULT 13
AF039752
LOCUS AF039752 1878 bp mRNA VRT 18-AUG-1999
DEFINITION Gallus gallus histone deacetylase-2 mRNA, complete cds.
ACCESSION AF039752
VERSION AF039752.1 GI:2791685
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1878)
Takami, Y., Kikuchi, H. and Nakayama, T.
Chicken histone deacetylase-2 controls the amount of the IgM
H-chain at the steps of both transcription of its gene and
alternative processing of its pre-mRNA in the DT40 cell line
J. Biol. Chem. 274 (34), 23977-23990 (1999)
93377029
2 (bases 1 to 1878)
Takami, Y.
Direct Submission
Submitted (23-DEC-1997) Biochemistry, Miyazaki Medical College,
Kiyotake Kihara 5200, Miyazaki 889-16, Japan
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REFERENCE 1 (bases 1 to 2073)
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
JOURNAL Putative histone deacetylase HDAC1 from Drosophila melanogaster
TITLE Unpublished
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
JOURNAL 2 (bases 1 to 2073)
AUTHORS Johnson,C.A., White,D., O'Neill,L.P. and Turner,B.M.
JOURNAL Submitted (26-SEP-1997) Anatomy, Univ. of Birmingham, Birmingham
B15 2TT, U.K.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:17:23 ; Search time 125.93 Seconds
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23	152.8	8.5	379	18	AAAT86372	Partial cDNA encod
24	140	7.8	375	18	AAAT86373	Human polynucleoti
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ALIGNMENTS

RESULT 1

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XX AAF80351;

XX 29-JUN-2001 (first entry)

XX Nucleotide sequence of a histone deacetylase designated ATRPD3B.

XX Histone deacetylase; ATRPD3B; gene expression; transgenic plant;
XX HDAL; ethylene-responsive phenotype; hypocotyl elongation; ds.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

XX CDS 121..1536

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XX WPI; 2001-258457/27.

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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 89.2%; Score 1606.4; DB 21; Length 1609;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 24 cttctcaggcattgtgacacaaattttgtctcgtagtaaaacttgggaatagagagaga 83
|||||
Db 1 cttctcaggcattgtgacacaaattttgtctcgtagtaaaacttgggaatagagagaga 60
|||||
QY 84 ctctcagtgagagagagattctgagtaaacgagagagagagagagagagagagagagagat 143
|||||
Db 61 ctctcagtgagagagagattctgagtaaacgagagagagagagagagagagagagagagat 120
|||||
QY 144 ctctctgcgttcgggacccgagcgagcgttaagcggcgagtcagttacttctacgagccgac 203
|||||
Db 121 ctctctgcgttcgggacccgagcgagcgttaagcggcgagtcagttacttctacgagccgac 180
|||||
QY 204 gatcggaactactactacggtcaaggccacccgatgaagcctccacggatccggtatggc 263
|||||
Db 181 gatcggaactactactacggtcaaggccacccgatgaagcctccacggatccggtatggc 240
|||||
QY 264 tcatagcctaatactactatcacctcacccgttcggttagaataacagtcgacctagcct 323
|||||
Db 241 tcatagcctaatactactatcacctcacccgttcggttagaataacagtcgacctagcct 300
|||||
QY 324 cgtcgaacctccgatatcggccgattccattcgcggagtgatgttgacttctcctcctc 383
|||||
Db 301 cgtcgaacctccgatatcggccgattccattcgcggagtgatgttgacttctcctcctc 360
|||||
QY 384 cgttccgcggaatctatggggatccttcggtgcgcgaacacccaaagcgaattcaatgt 443
|||||
Db 361 cgttccgcggaatctatggggatccttcggtgcgcgaacacccaaagcgaattcaatgt 420
|||||
QY 444 cggtagagattgctcgtcttcgagcgagacttttgatttttccgtgttcgcgcggagg 503
|||||
Db 421 cggtagagattgctcgtcttcgagcgagacttttgatttttccgtgttcgcgcggagg 480
|||||
QY 504 ttctattggtgctgcgtcctcaaatataacagacagagcgtgatcgtatcgaattgggg 563
|||||
Db 481 ttctattggtgctgcgtcctcaaatataacagacagagcgtgatcgtatcgaattgggg 540
|||||
QY 564 cggtagggttcacacatgctaagaaagcgaggttcctgggttttgcgtatgtaaacgacat 623
|||||
Db 541 cggtagggttcacacatgctaagaaagcgaggttcctgggttttgcgtatgtaaacgacat 600
|||||
QY 624 cgtgctagggattctggagttgctcaagatgtttaagcgggttctctacatagatttga 683
|||||
Db 601 cgtgctagggattctggagttgctcaagatgtttaagcgggttctctacatagatttga 660
|||||
QY 684 tgtccaccatggagatggagtggaagaagcgttttacaccactgataagttatgactgt 743
|||||
Db 661 tgtccaccatggagatggagtggaagaagcgttttacaccactgataagttatgactgt 720
|||||
QY 744 tctttccacaaatttggggacttttcccgaggactgttccacataaagagatgttgggc 803
|||||
Db 721 tctttccacaaatttggggacttttcccgaggactgttccacataaagagatgttgggc 780
|||||
QY 804 tgaagaaagggaataactatgctctaaatgttccactaaacagatggtatggcgatgaaag 863
|||||
Db 781 tgaagaaagggaataactatgctctaaatgttccactaaacagatggtatggcgatgaaag 840
|||||

Db 686 atattgatatccacacaggggagtgagtgagggaggggattttatgtactacgaggggtta 745
 Qy 737 tgactgtttcttccacaaaattgggagacttttcccgaggaactgggtcacataagagatg 796
 Db 746 tgactgtctgtttcataaaatttggtgattactttcccgtagaggtcacattcagata 805
 Qy 797 ttggcgtgaaaaaggaataactactctctaaattgttccactaaaacgattggtatgacg 856
 Db 806 taggttatggtagcggaagtactattctctcaatgtaccactggtatggaatogatg 865
 Qy 857 atgaaagtcccgagctgtgttttagaccttcttccagaaggttatggaagtgtatcagc 916
 Db 866 atgagagctatcatctgtttatcaagcccatcattggggaaggttatgaaatttccgac 925
 Qy 917 cagagggcagttgtctcagttgtgtgctgactccttaagtgtgtgactcgtgtggtgct 976
 Db 926 caggggctgtgtattgcaatgtgtgtgactcctctatctgggagtcggttaagtgtct 985
 Qy 977 tcaactatcagtcgaaggtgcacgctgattgcttcgttctttaaagatcttcaaacgttc 1036
 Db 986 tcaactttcaatcaaggtcattgctgagtcgctcaaatattatgagatcgttcaatgttc 1045
 Qy 1037 ctctcagttgttgggtggtgaaggtatactattcgaataattgtcccggtgtgtgtgt 1096
 Db 1046 cctcactgtcttgggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1105
 Qy 1097 atgagactgcagttgt 1156
 Db 1106 acgagactgaggt 1165
 Qy 1157 ttgagttattcggccagattatcagtttctcatgttcgacccaagtccttatggagaattaa 1216
 Db 1166 atgaactttggtccagactatacattcactcactgttctcgaatgaacatggaataaga 1225
 Qy 1217 acagcccaagatagtagagagataaggaacacggtgtgtgtgtgtgtgtgtgtgtgt 1276
 Db 1226 attctgtcagatgtgtgaagagattcgcgaatgaccttctccacaattctcttaagcttc 1285
 Qy 1277 tacagcacttagctcagtttcagcacacacaccag 1315
 Db 1286 agcatgtccaaagtaccatttcaggaaagaccactgt 1324

RESULT 8

ID AA258259 standard; cDNA; 1990 BP.
 XX
 AC AA258259;
 XX
 DT 08-MAY-2000 (first entry)
 XX
 DE Rice histone deacetylase gene 1 (HDI) cDNA contig.
 XX
 KW Chromatin associated protein; histone deacetylase gene 1: HD1;
 XX rice; transgenic plant; transcription regulation; ss.
 OS Oryza sativa.

Key Location/Qualifiers
 CDS 3..1484
 /tag= a
 /partial

W0200004177-A1.

PD 27-JAN-2000.
 XX
 PF 13-JUL-1999; 99WO-US15807.
 XX
 PR 14-JUL-1998; 98US-0092841.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX

PI Cahoon RE, Vollmer SJ;
 XX WPI: 2000-182439/16.
 DR P-PSDB; AA58828.
 XX
 PT New nucleic acid fragment useful as probes and primers, for
 PT transforming plants -
 XX
 PS Claim 3; Page 24; 36pp; English.
 XX
 CC The present sequence is that of a contig encoding a portion
 CC (see AA58828) of rice histone deacetylase 1 (HDI), a chromatin
 CC associated protein. The contig was obtained from cDNA clones
 CC isolated from rice callus, 15-day-old leaf and 15-day-old seedling
 CC cDNA libraries on the basis of homology to other plant histone
 CC deacetylases. The invention relates to isolated rice, soybean and
 CC wheat nucleic acid fragments encoding HD1. It also relates to the
 CC construction of a chimeric gene encoding all or a portion of HD1,
 CC in sense or antisense orientation, where expression of the chimeric
 CC gene results in production of altered levels of HD1 in a
 CC transformed host cell. The availability of nucleic acid sequences
 CC encoding (portions) of histone deacetylase proteins will facilitate
 CC studies of global transcriptional regulation in eukaryotic cells,
 CC and will also provide mechanisms to control transcriptional gene
 CC regulation in plants.
 XX
 SQ Sequence 1990 BP; 502 A; 494 C; 518 G; 476 T; 0 other;

Query Match 28.8%; Score 518.8; DB 21; Length 1990;
 Best Local Similarity 66.5%; Pred. No. 1.2e-134;
 Matches 777; Conservative 0; Mismatches 382; Indels 9; Gaps 2;

QY 185 gttactctcagcgagcgagcagctgagagactactactactcagtcagcagccaccccgatgaagc 244
 Db 1 gctactctcagcgagcgaggtgggaactactactactcagtcagcagccaccccgatgaagc 60
 QY 245 ctacccgagctcctgctgctcagctcagctcagctcagctcagctcagctcagctcagctcagct 304
 Db 61 cgcacgcaccccgagtgacccacgcgctgctcagctcagctcagctcagctcagctcagctcagct 120
 QY 305 aatcagtcgctcctgagctgagcgcctcagctcagctcagctcagctcagctcagctcagctcagct 364
 Db 121 aggtgctcagccaccccgcgcgacgcgacctcgcgctcagctcagctcagctcagctcagctcagct 180
 QY 365 atgtgactcct 424
 Db 181 acgtgctcct 234
 QY 425 acctaaaggcattcaatgctggtgaggtgctcctcctcctcctcctcctcctcctcctcctcctcctcct 484
 Db 235 cgtcgaagcgttcaacgctcgcgaggaactgcctcctcctcctcctcctcctcctcctcctcctcctcct 294
 QY 485 ggcgtgctcgcgcgaggttctattggtgctgcctcctcctcctcctcctcctcctcctcctcctcctcct 544
 Db 295 gccagacctacgcggggtcgcgctgc 351
 QY 545 atatcgctataattggggcggtgggttcacacatgctaaagaagcagagcttctgggt 604
 Db 352 acatcgctataattggggcggtgggttcacacatgctaaagaagcagagcttctgggt 411
 QY 605 ttgtctatgaaacgacatcgtgtagggattctgaggtgctcagagattttaagcggtg 664
 Db 412 tctgctacgcaacgacatcgtctcgcctcctcctcctcctcctcctcctcctcctcctcctcctcct 471
 QY 665 ttctctacatagattatgtatgcacacatgagatgagtgagtgagtgagtgagtgagtgagtgagtgagtg 724
 Db 472 ttctctatggtatcagatcaccatggggtggtggtggtggtggtggtggtggtggtggtggtggtggt 531
 QY 725 ctgataagattatgactgtttcttccaaaaattggggactttttccacaggaacggttc 784
 Db 532 cggacaggggtgagacggtctgtctccacagtttggggattatttcccggggaccgggtg 591

Db 474 gcagatgcataatttaattgttgagaaagattgtccagcgtttgatggactcttgagtt 533
 QY 483 ttgcggtgctccgcggaggttctattgtgctgcgtccaaattaaacagacagcgc 542
 Db 534 ttgcagctctcaactggcgttcagttgctgagcgtgaagttaaaccgcaacagac 593
 QY 543 tgatagctcatcaattggcggcgttccaccatgctaaagaaagcagcgtctctgg 602
 Db 594 tgatagcgttaattggcggaggttacatcatgctaaagaaatcacagatcagc 653
 QY 603 gtttgcctatgaacacacatgctgtagggattctggagttgctcctcaagatgttaagcg 662
 Db 654 attctgttaacgttaattgtgttgcctcctggaattactaaagtatcatcagag 713
 QY 663 gttctctacatagattatgtccaccatggagatggagtggaagaaagcgtttttacac 722
 Db 714 agtcctatatgatatagattatcattcatcattggtggtgttgagaaagcgtttttatc 773
 QY 723 cactgtagagttatgactgtttctcccaaaattggggagctttttcccgagaaactgg 782
 Db 774 aacagatcgtgtaatgacgttaccatcccaataatggggaatactttctcggcacag 833
 QY 783 tcacataagagatttggcgtgaaagaaagaaatactatgctcctaattgtccactaaa 842
 Db 834 agactgagggatattggtgctggaagaaagcaaatactatgctgtcaattttccaatgtg 893
 QY 843 cgtatgtagacatgaagatttccgcagcttgttttagacctctatccagaaaggttat 902
 Db 894 tgatggtatagatagatgcatatggcgagatatttaacgcttattctccaaaggatg 953
 QY 903 ggaagttatcacgcagcagcaggtttcttcaggtggtgctgactccttaagtgtga 962
 Db 954 ggagatgtatacaactagtgctgtgtattacagtggtgagactcattatctgtga 1013
 QY 963 tcggttggttgcctcaactatcagtcaggggtcagcgtgattgccttcggttcttaag 1022
 Db 1014 tagactgggttgttcaactcaacagtcacagtcacaggtcatgctaaatgtgagaagtgtaaa 1073
 QY 1023 atcttaacacgttctctcatggttgggttgggtgaaggttactactattcgaagtgtgc 1082
 Db 1074 aacttttaacttaccattactgattggtgagaggtggtacacaaatcgtaatgtgc 1133
 QY 1083 ccgttgtggttattgagactgcagttgctgttggagtagagcggacacaaactccc 1142
 Db 1134 tcgattgtggacatgagatgcagtcgagttgctcctgtgttgagattcccaatgagttgcc 1193
 QY 1143 ttcaaatgagattttgagattttcgccagattatcagcttcatgctgacccaagttcc 1202
 Db 1194 atataatgattactttgagatttttgaccagactcacaactgcatattagttcctcaa 1253
 QY 1203 tatggagaatttaaacacgcaccaagatatggagaggtatgaagaaacacgttgcgtggaaca 1262
 Db 1254 catgacaaccagaaactccagaaatatatggaaaagataaaacagcgtttgtttgaaa 1313
 QY 1263 actttcgggactataacacgcacctagctccagtttcagtttcagcacacacacag 1315
 Db 1314 ttgycgcatgttacctatgcacctgtgtccagatgcaagctattccagaag 1366

RESULT 12

AAC89555

ID AAC89555 standard; DNA: 1985 BP.

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

XX AC AAC89555;

OS Homo sapiens.
 XX WO200071703-A2.
 PN 30-NOV-2000.
 PD 03-MAY-2000; 2000WO-IB01252.
 PF 03-MAY-1999; 99US-0132287.
 PR (METH-) METHYLGENE INC.
 PA Macleod AR, Li Z, Besterman JM;
 PI WPI: 2001-016407/02.
 XX P-PSDB; AAB49955.
 DR Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal -
 PS Disclosure; Page 53; 125pp; English.
 XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia.
 XX Sequence 1985 BP; 626 A; 360 C; 454 G; 545 T; 0 other;

Query Match 24.7%; Score 444.6; DB 22; Length 1985;
 Best Local Similarity 61.4%; Pred. No. 6.2e-114; Indels 6; Gaps 1;
 Matches 733; Conservative 0; Mismatches 454;

QY 123 ggaggcagacgaagcggcatctctgcgtcgggacccgacgcgagcgttaagcggcag 182
 Db 180 ggtggcggcgttggcgggagccatggtgacagtcagagcggcgaacaaagc 239
 QY 183 cagttactctacagccgacgacgtcggagactactactactactactactactactact 242
 Db 240 ctgctactactacagcgggtgattggaattattattattattattattattattatt 299
 QY 243 gctcaccggtcgtggtgctcagcctaatcattcattcattcattcattcattcattc 302
 Db 300 gctcattagatccgatgacccataactgtgtgtaattggttattggttattggttatt 359
 QY 303 agaaatcagtcgcctcagcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtcgcgtc 362
 Db 360 ggaatatatagcccccataaagccactgccgaagaaagacaaatatacacagtatga 419
 QY 363 gtatgttgactctcgtcttcgttttcgcgggaattctatggtggtggtggtggtggtg 422
 Db 420 gtatatcaatttctacggtcctaataagaccagataacatg-----tctgagtagtaa 473
 QY 423 aaacctaaagcgttcaatgctcgttgaggattgctcgtcgtcgtcgtcgtcgtcgtcgt 482
 Db 474 gcagatgcataatttaattgttgagaaagattgtccagcgtttgatggactcttgagtt 533
 QY 483 ttgcgtgcttcgcggaggttctattggtgctgcgtcgtcgtcgtcgtcgtcgtcgtcgtc 542
 Db 534 ttgcagcttcaactcggcgttccagttggtgaggtggtgaggtggtgaggtggtgaggt 593
 QY 543 tgatagcgtcatcaattggggcgttgggttccaccatgctaaagaaagcagcgttctg 602
 Db 594 tgatagcgttgaattggcgtgaggtattacatcatgctaaagaaatcacagatcagc 653
 QY 603 gtttgcctatgaacacacatgcttagggattctgaggttctgaggttctcaagatgtttaagcg 662
 Db 654 attctgttaacgttaattggtgcttgccatccttggtggtggtggtggtggtggtggtg 713

QY 1134 caaacctcccttaccatagatattttagtatttgcggccagattatacagcttcattgtcga 1193
 Db 978 tgagctccatacaatgactactttgaatactttgaccagatttcaagctccacatcag 1037
 QY 1194 ccaagctcatgagagaatttaaacacgcccgaagatataggagataaagaaacaglt 1253
 Db 1038 tccctccaatagactaacagacacgcaatgactacctggagagatacaaacagcgaact 1097
 QY 1254 gctgggaacacttcgggagactatacaacgacactagcgtccagtttcag 1302
 Db 1098 gtttgagaaccttagaattcgtccgacacgacctgggtccaaatgcag 1146

RESULT 15

AAC89554

ID AAC89554 standard; DNA; 1611 BP.

AC AAC89554;

XX 08-MAR-2001 (first entry)

XX Human histone deacetylase HDAC-1 coding sequence.

XX Histone deacetylase: HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
 KW HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
 KW gene therapy; ds.

XX Homo sapiens.

XX WO200071703-A2.

XX 30-NOV-2000.

XX 03-MAY-2000; 2000WO-IB01252.

XX 03-MAY-1999; 99US-0132287.

XX (METH-) METHYLOGENE INC.

XX Macleod AR, Li Z, Besterman JM;

XX WPI; 2001-016407/02.

XX P-PSDB; AAB49954.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal -

XX Disclosure; Page 50-51; 125pp; English.

XX The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia.

XX Sequence 1611 BP; 428 A; 385 C; 440 G; 358 T; 0 other;

Query Match

Best Local Similarity 24.3%; Score 436.6; DB 22; Length 1611;
 Matches 704; Conservative 0; Mismatches 419; Indels 6; Gaps 1;

QY 174 gcggcgagtcagttacttctacgagccgacgactcagactactactacggtcaaggcca 233
 Db 134 gaggaaagctgttactactacgacgagggtgttgaaataactattatggaaggaagcca 193
 QY 234 ccgatgaagcctaccggatccggtatggtcctatagcctaatcattcactatcactccca 293
 Db 194 cccaatgaagcctaccgaatccgcatgactcataattgtcgtcactatggtctcta 253
 QY 294 ccgtcgttagaaatcagtcgacctagctcgtcagcctcagctatcgcgcgattcca 353

Search completed: March 8, 2002, 23:41:43
 Job time: 1460 sec

Db 254 cggaaaaatgaaaatctatccctcacaaagccaatctgagagatgaccaagtacca 313
 QY 354 ttccgcggagtagttgacttctcgtctccgtttccggttccggaatctatggcgatctte 413
 Db 314 cagogatgactacataaattcttgcctccatccgtccagataacatctgcggagtacag 373
 QY 414 cgtgcacgaaacctaaaggcattcaatctcgtcgtgagagattgtcctctccgcaggact 473
 Db 374 c-----aagcagatgcagagattcaacgttggtagagactgtccagtattcgalggcct 427
 QY 474 ttttgattttgcogtgcctccgcggaggtttctatttggtgctccgctcaaatataacag 533
 Db 428 gtttgagttctgcagttgtctactcgtggtctcgtggaagtgctgtgaactataa 487
 QY 534 acaggacgtgatatcgtatcaattggggcggtgggtccaccatgcttaagaaagcga 593
 Db 488 gcagcagacgacatcgtcgtgaattgggtgggtgggtgggtgggtgggtgggtgggtgggt 547
 QY 594 ggcttcgggtttgctatgtaaacgacatcgtcgtcagggattctcggagtgtcgaagat 653
 Db 548 ggcattcgtctgttacgtcaatgatcgtcttgccatcctggaactgtcaagta 607
 QY 654 gtttaagcgggttctctacatagattgattgctccaccatgagatggagtggaagcga 713
 Db 608 tcaccagaggtgctgtacattgacattgattcaccatggtgacggtggaagagdc 667
 QY 714 gttttaccactgataagattgactgtttcttccacaaatttggggactttttccc 773
 Db 668 ctctacaccgagaccgggtcagctgtcttcttcaagatgagagagacttccc 727
 QY 774 aggaactggtcacataagagattgttgcgtgaaagaaagaaatactatgctctaaatgt 833
 Db 728 aggaactgggacctacgggatalcggggtcgcaagcgaagattatctgtttaacta 787
 QY 834 tccactaaacgatggtagcagatgaaagtgttcgcagctgtgttaagacctttatcca 893
 Db 788 ccgcctcagacgggattgatgcagctcctatgagccattttcaagcggctcatgtc 847
 QY 894 gaaggttatggaagtgtatcagccagagagcagttgtcttcagttggtgtgctactcct 953
 Db 848 caaagtaatggagatgttccagcctagtgcgggtggtctacagttggtgctcagactcct 907
 QY 954 aagtggtgacggttgggttcttcaactatcagtcagtcagtcagtcagtcagtcagtcagtc 1013
 Db 908 atctgggagtcggttaggttctcaatcctaactataaaggacacgccaagtggtgga 967
 QY 1014 gttcttaagatcttacaacggttctcctcagttggtgtggtggtgaagggtatactattcg 1073
 Db 968 attgtcagaagcttcaacctgctatgctgatgctggagggcgggtgttaccaccttcg 1027
 QY 1074 aaatgttcccggttgcgtgttatgagactgcagttgctgttgagtagagagccggaaca 1133
 Db 1028 taagttcccggtgctggacatagagacagctgtggcctgagacgagagatccctaa 1087
 QY 1134 caaactcccttacaatgagtagttttgagatttccggccagattatcagcttcatgtcga 1193
 Db 1088 tgagcttccatacaatgactactttgaatactttggaccagatttcaagctccacatcag 1147
 QY 1194 cccaagtcctatggagaatttaaacacgcccgaagatatggagagataaagaaacagctt 1253
 Db 1148 tccctccaatagtaaccaggaacacgaatgagtagctgtgagagatcaaacagcagact 1207
 QY 1254 gctggaaacaacttcgggactataacacgacacgtcagctcagtttcag 1302
 Db 1208 gtttgagaaccttagaatgctgcgcgacgacctggggtccaaatgcag 1256

Dbb 1330 tcctg 1334

RESULT 4

```

US-09-282-305-3
; Sequence 3, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:
; APPLICANT: Baldwin, Donald A.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Crane, Virginia C.
; TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
; FILE REFERENCE: 5718-44,
; CURRENT APPLICATION NUMBER: US/09/282,305
; CURRENT FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/080,563
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29)..(1084)
US-09-282-305-3

```

Query Match	24.5%	Score 441.4;	DB 4;	Length 1475;
Best Local Similarity	71.9%	Pred. No. 1.1e-116;		

570	ggttcaccatgctgaagaaaagcaggcctctggttttgctatgtaaacgacatcgtct	629
QY		
160	gcccacacacccgaagagcgaggcctccgggtctctgctacgtcaacgacatcgtcct	219
Db		
630	agggattctggagttgctcaagatgtttaagcgggttctcacatagatattgatccca	689
QY		
220	cgcctctctcgagctctccaagttccacaggcgtgctctatatgtagacattgatccca	279
Db		
690	ccatggagatggagtggaagaagcgttttacaccactgatagatttatgactgtttcttt	749
QY		
280	ccatggagatggcgtggagggcctcttctcactacaacccgagtcagtgttctctt	339
Db		
750	ccacaaaattggggacttttcccaggaactggtccacataagagatgttggcgcctgaaaa	809
QY		
340	tcacaagtatggggatttttccctgctcattggacatcatcactgacgttgggcagccga	399
Db		
810	agggaataactatgctctaaatgttccactaaaacgattggtatggacgatgaaagtctccg	869
QY		
400	agggaagcatatgctctgaatgttcccctgagtgatgggtatcgatgaaccaccttcg	459
Db		
870	cagctgttttagacctttatccgaaggtttatggaagtgtatcagccagagcagttgtt	929
QY		
460	tggctgtttcaatgcataagaagttatggaggtttatcagccagacgtggttgt	519
Db		
930	tcttcagtggtgctgactccttaagtgtgtatcggttggttgcctcaactatcagt	989
QY		
520	cctccaatgcggagcgtgactcttggctggagacaggttaggttgcctcaacgtctgt	579
Db		
990	caagggtcacgctgattgcctcggttcttaagatcttacaacgcttctctcatgtgtt	1049
QY		
580	gaagggtcatgctgactgcctcgtttccttaggtctgcacatgttctaagtgtgtttt	639
Db		
1050	gggttggtgaagggtatactattccgaaattgttgcctgttgcgtgttatgagactcagt	1109
QY		
640	agggtggtggaggttacaccatcagaaatgttgacgctgctggtgctacgagaccgcagt	699
Db		
1110	tactgttgagtagagccgggacacaaactcccttacaatgagtattttgaqtattcgg	1169
QY		
700	tactgttgaggtgaacctgatacaagctgccttacaatgattactatgactgtgtgg	759
Db		

[illegible]

RESULT

```

US-08-528-255A-2
Sequence 2, Application US/08528255A
Patent No. 5659016
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : FURUKAWA, YOICHI
TITLE OF INVENTION: RBDL PROTEIN AND DNA
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/528,255A
FILING DATE: September 14, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
NAME: ferrylene F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: Furuya Case 1335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2111
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
LIBRARY: human fetal lung cDNA library
FEATURE:
NAME/KEY: CDS
LOCATION: 64..1512
IDENTIFICATION METHOD: experimental examination
US-08-528-255A-2

```


Query Match 24.2%; Score 435; DB 1; Length 2111;
Best Local Similarity 62.3%; Pred. No. 9.2e-115;
Matches 703; Conservative 0; Mismatches 420; Indels 6; Gaps 1;

QY 174 gcggcagtcagttactctacagccgagcagctgagagactactactacaggtcaaggcca 233
DB 87 GAGGAAAGTCTGTACTACTACGCGGATGTTGGAATATTACTATTATGGACAAAGGCCA 146

QY 234 cccgatgaagccctccagcagctcgtatggtctatagctcctaaatcattcactatcacctcca 293
DB 147 CCCAATGAAGCCCTCACCGAATCCGCATGACTCATATTTGCTGCTCAACTATGCTCTCTA 206

QY 294 cccgccttagaatacagtcgctcagctcagctcagcctcagctcagctcagctcagctcag 353
DB 207 CCGAAAAATGGAATCTATCGCCTCACAAAGCCAAATGCTGAGGAGATGACCAAGTACCA 266

QY 354 ttccgcgagtagtctgctcctcctcctcctcctcctcctcctcctcctcctcctcctc 413
DB 267 CAGCGATGACTTAATTTCTTGGCTCCATCCGTCAGATACATGTCGGAGTACAG 326

QY 414 cgtgcacgaacctaagcgattcaatgctcgtgaggttctcctgctcctcagcgact 473
DB 327 C-----AAGCAGATCCAGAGATCAACGTTGCTGAGGACTGTCCAGTATTCGATGGCT 380

QY 474 ttttgatttttgcgtgctcgc 533
DB 381 GTTTGAGTTCTGTCACTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 440

QY 534 acaggacgtgatctcgtatcaatgctcgtgaggttctcctgctcctcagcgact 593
DB 441 GCAGCAGAGCGGATCGCTGTAATTTGGGCTGGGCGCCGTCACCATGCAAGAAAGTCCCA 500

QY 594 gctctcgtggtttgctatgataacacacatgctgaggttctcgtgaggttctcgtgaggt 653
DB 501 GGCATCTGGCTTCTGTAGTCAATGATATCGTCTTGGCCATCCCTGGAATCTGCTAAAGTA 560

QY 654 gtttaagcgggttctcagatagatttgatgccaccatgagatgagatgagatgagatgag 713
DB 561 TCACCAGAGGGTCTGTACATTGACATTGATATTCACCATGCTGAGCGGCTGGAAGAGGC 620

QY 714 gtttacacactgagtagttagttagttagttagttagttagttagttagttagttagttag 773
DB 621 CTCTACACACGAGCGGGTGTAGTGTGCTTCTTCAATAAGTATGGAGAGTACTTCC 680

QY 774 aggaactggtcacataagagatgttgcgctgataaagagagagagagagagagagagag 833
DB 681 AGGAATGGGACCTACGGGATATCGGGCTGCCAAGGACAGATATTATGCTGTTAACTA 740

QY 834 tccactaacgtagttagttagttagttagttagttagttagttagttagttagttagttag 893
DB 741 CCGGCTCCGAGAGCGGATGATGACGAGTCTTATGAGGCAATTTTCAAGCCGGTCAATGC 800

QY 894 gaaggtatggaagttagttagttagttagttagttagttagttagttagttagttagttag 953
DB 801 CAAAGTAATGGAGATGTTCCAGCCTAGTGGTGGTCTTACAGTGTGGCTCAGACTCCCT 860

QY 954 aagtggtgagcgttgggtggttgcctcaactatcagtcagaggtcagcgtgattgcttcg 1013
DB 861 ATCTGGGATCGGTAGTGTGCTCAATCTAATCTAAGTATCAAGGACACCCCAAGTGTGGA 920

QY 1014 gttcttaagatttacaacgctcctcctcctcctcctcctcctcctcctcctcctcctc 1073
DB 921 ATTGTCAAGAGCTTTAACTGCTTATGTGATGCTGGGAGCGGGTGTACACCATTCG 980

QY 1074 aaatgttgcggttgggtttagttagttagttagttagttagttagttagttagttagttag 1133
DB 981 TAACGTTGCCGGTGCAGACATATAGACAGCTGTGGCCCTGGATACGGAGATCCCTAA 1040

QY 1134 caaacctccttacaatgagattttgagttatcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1193
DB 1041 TGAGCTCCATACAACTACTTGTGAATTTGAGGACAGATTTCAAGCTCCACATCAG 1100

QY 1194 cccaagctctatgagaatttaaacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1253

DB 1101 TCCTTCCATATGACTAACCAACACACGAATGAGTACCTGGAGAAGATCAACACGCGACT 1160
QY 1254 gctgaacaacttttcggaactaatacacacacacacacacacacacacacacacacac 1302
DB 1161 GTTTGAGAACCTTAGAATGCTGCGCGACGACCTGGGGTCCAAATGCAG 1209

RESULT 6
US-08-717-365-2
; Sequence 2, Application US/08717365
; Patent No. 5763182
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, YUSUKE
; TITLE OF INVENTION: RPDL PROTEIN AND DNA
; TITLE OF INVENTION: ENCODING THE SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLYNN, THIEL, BOUTELL & TANIS, P. C.
; STREET: 2026 Rambling Road
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49008-1699
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08717,365
; FILING DATE: 23-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/528 255
; FILING DATE: September 14, 1995
; APPLICATION NUMBER: JP6-227876
; FILING DATE: 22-SEPTEMBER-1994
; APPLICATION NUMBER: JP7-183763
; FILING DATE: 20-JULY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Terryence F. Chapman
; REGISTRATION NUMBER: 32549
; REFERENCE/DOCKET NUMBER: Furuya Case 1335
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 381-1156
; TELEFAX: (616) 381-5465
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2111
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: human fetal lung cDNA library
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 64..1512
; IDENTIFICATION METHOD: experimental examination
; US-08-717-365-2

Query Match 24.2%; Score 435; DB 1; Length 2111;
Best Local Similarity 62.3%; Pred. No. 9.2e-115;
Matches 703; Conservative 0; Mismatches 420; Indels 6; Gaps 1;

QY 174 gcggcagtcagttactctacagccgagcagctgagagactactactacaggtcaaggcca 233
DB 87 GAGGAAAGTCTGTACTACTACGCGGATGTTGGAATATTACTATTATGGACAAAGGCCA 146

Db 681 aaagggaagaaatattatgtctatcaacattccacttaaaagatgggatagatgacacta 740
QY 863 gtttcgcagctgttttagacctcttaccagaaggtttatgaaagtgtatcaagcagagg 922
Db 741 gctttactcgccttttaaaacaaattattgccaaggttgttgagacatatcgctggtg 800
QY 923 cagttgttctcagtggtgctgactccttaagtggtgagtggttggttgcctcaact 982
Db 801 ctatgttctcaatggtggtgctgattcattggtgaggtggtttaggtgcttcaatc 860
QY 983 tatcagtcgaaggtcagctgattgctccttggttcttaagatcttacaacgttctctca 1042
Db 861 tctctatgaagggcctgctgaatgtgtaagtttgcagaataatcaattcccttc 920
QY 1043 tgggtgtggtggtgaaggtatatactattcgaatgttgccgttgcgtggttatgaga 1102
Db 921 tggtaactggaaggtggtgatacacacagaaggagaatgtgacacgtgtgtggcgttgaa 980
QY 1103 ctgcagttgctgttgagtagagccgggacacaaacacccctcttacaatgatttttgat 1162
Db 981 ctggggtccttttagacacagaaactcccaaatgagattcccaaaaatgaatatattgat 1040
QY 1163 atttcggccagattatagcttctatgtcgaccccaagtcctatgagaaatttaaacacgc 1222
Db 1041 actttgctccagattatatactgaaagtcccaatttgaacatggacaaatttgaacagta 1100
QY 1223 ccaagatagtagagaggaagaaacacagctgtgtagaacaacttccggagactaatacacg 1282
Db 1101 agacctatctcagttccaaatgcaagtgcaagtgatgagagtttgcgtgtacatacagcatg 1160
QY 1283 cactcagctcagtttccagcacacacaccagtcacatcgagtttggacgagccggag 1342
Db 1161 ctcttggttccaaatgcaagaggttctctccgatttttatatccggagactttgatgaag 1220
QY 1343 atgacatgga 1352
Db 1221 atgaattgga 1230

RESULT 8

US-08-998-416-317

; Sequence 317, Application US/08998416

; Patent No. 6239264

; GENERAL INFORMATION:

; APPLICANT: philippsen, Peter

; APPLICANT: Pohlmann, Rainer

; APPLICANT: Steiner, Sabine

; APPLICANT: Mohr, Christine

; APPLICANT: Wendland, Jürgen

; APPLICANT: Knechtle, Philipp

; APPLICANT: Reibschung, Corinne

; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII

; NUMBER OF INVENTION: AND USES THEREOF

; NUMBER OF SEQUENCES: 1152

; CORRESPONDENCE ADDRESS:

; ADDRESS: No. 6239264artis Corporation

; STREET: 3054 Cornwallis Road

; CITY: Research Triangle Park

; STATE: No. 6239264th Carolina

; COUNTRY: USA

; ZIP: 27709

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/998,416

; FILING DATE: 24-DEC-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: CH 0016/97

; FILING DATE: 31-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy

; REGISTRATION NUMBER: 38,241

; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8587

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 317:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 841 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: PAGI256UP

US-08-998-416-317

Query Match

Best Local Similarity 10.2%; Score 184; DB 4; Length 841;

Matches 337; Conservative 0; Mismatches 215; Indels 4; Gaps 2;

QY 553 atcaattggggcgtgggttcacacatgctaaagaaagcagaggtctctgggtttgttat 612
Db 2 ATCAACTGCTCGGGCGGCTGCACCCAGCAAGAGCAATCTCTCGGGGTTCGTGTAC 61
QY 613 gtaaacacatctgctagggattctggagttgctcaagatgtttaagcgggttctctac 672
Db 62 GTGACGACATTTGTTGGCGATTCTGAATCTGCTGCCCTACCAACCCACGCGGTTCGTAC 121
QY 673 atagatatgtatccaccatggagatggagtgaaagcgttttaccacactgagaga 732
Db 122 ATTGACATTGATCTGCCACCGGAGCGGTGTCCAAAGAGCATCTTACACTACTGACCGC 181
QY 733 gttatgactgtttcttcacacaaat---ttggggactttttccacaggaaactggttcacata 789
Db 182 GTGTTTCACGGTCTCGTTCACAAAGTACAATGCTGAGTGTTCGCGGGAACGGGGATTG 241
QY 790 agagatgttgcgctgaaaaaggggaaataactatgctctaaatgttccactaaacagatgt 849
Db 242 GATGATCGGATGCTCGCGCGCAAGCACTTTTCGCTGAATGTGCCCTCAATGACCGC 301
QY 850 atggaacatgaaagtctccgagctgttttagacctcttaccagaaaggttatgaaagt 909
Db 302 ATCGATGATGATCTGATACATCACTTATTAAAGACCATCATAGACCCCTACTTACATCA 361
QY 910 tatcagccagagggcagttgttctcaagtgtggtgctgactccttaagtgtgagtggtg 969
Db 362 TACAAGCCACACAGTAATTATTTCAGCAATGTGGAGCAGACTCTTTGGGGCATGACAGACTG 421
QY 970 gtttgcctcaactatcagtcagtcaggggtcaagctgattgcttcggttcttaagatcttac 1029
Db 422 GGGTGTTCATTAATCTAAATATCAGAGCCCGGCGGAGTGCCTCAATTTGTGAAG-TCGTTTC 480
QY 1030 aacgttctctcatgggtgttgggtgaaagggtatattcgaatgttgcgcgttgc 1089
Db 481 GGGATACCTATGCTATGTGTCGTGGTGGAGGTGTACACCCCGAGAAATGTGTGCGGGCTA 540
QY 1090 tgggttatgagagatg 1105
Db 541 TGGAGTACGAGAGACAG 556

RESULT 9

us-09-013-634-1

; Sequence 1, Application US/09013634

; Patent No. 5945307

; GENERAL INFORMATION:

; APPLICANT: M. Alexandra Glucksmann and Keith Robison

; TITLE OF INVENTION: LIGAND RECEPTORS AND USES THEREFOR

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,634
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Attorney, Jean M. Silveri
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 184..1194
US-09-013-634-1

Query Match 4.2% Score 75; DB 2; Length 2581;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 aaaaaaaaaaaaaaaaaagggcgccgtctagagatccaagcttacgacgcg 1785
|||||
Db 2497 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGATCCAAGCTTACGCGG 2556
|||||
QY 1786 tgcacgcgcgtcat 1800
|||||
Db 2557 TGCATGCGAGCTCAT 2571

RESULT 10
US-09-118-442-29/c
Sequence 29, Application US/09118442B
Patent No. 6197561
GENERAL INFORMATION:
APPLICANT: Martino-Catt, Susan J.
APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry R.
APPLICANT: Wang, Xun
APPLICANT: Bowen, Benjamin A.
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
FILE REFERENCE: 0706
CURRENT APPLICATION NUMBER: US/09/118,442B
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/055,446
EARLIER FILING DATE: 1997-08-11
EARLIER APPLICATION NUMBER: 60/055,526
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: 60/053,944
EARLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1330
TYPE: DNA
ORGANISM: Zea mays
US-09-118-442-29

Query Match 4.0% Score 72; DB 4; Length 1330;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 aaaaaaaaaaaaaaaaaagggcgccgtctagagatccaagcttacgacgcgtgc 1788
|||||
Db 94 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGATCCAAGCTTACGTACGCGTGC 35
|||||
QY 1789 atgcgcgcgtcat 1800
|||||
Db 34 ATGCGAGCTCAT 23

RESULT 11
US-09-677-064-29/c
Sequence 29, Application US/09677064
Patent No. 6291224
GENERAL INFORMATION:
APPLICANT: Martino-Catt, Susan J.
APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry R.
TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
FILE REFERENCE: 0706D
CURRENT APPLICATION NUMBER: US/09/677,064
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: 60/055,446
PRIOR FILING DATE: 1997-08-11
PRIOR APPLICATION NUMBER: 60/055,526
PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 60/053,944
PRIOR FILING DATE: 1997-07-28
PRIOR APPLICATION NUMBER: 09/118,442
PRIOR FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1330
TYPE: DNA
ORGANISM: Zea mays
US-09-677-064-29

Query Match 4.0% Score 72; DB 4; Length 1330;
Best Local Similarity 100.0%; Pred. No. 5.3e-11;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1729 aaaaaaaaaaaaaaaaaagggcgccgtctagagatccaagcttacgacgcgtgc 1788
|||||
Db 94 AAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGATCCAAGCTTACGTACGCGTGC 35
|||||
QY 1789 atgcgcgcgtcat 1800
|||||
Db 34 ATGCGAGCTCAT 23

RESULT 12
US-08-383-756-1
Sequence 1, Application US/08383756
Patent No. 5654495
GENERAL INFORMATION:
APPLICANT: Dehesh, Katayoon
APPLICANT: Voelker, Toni Alois
APPLICANT: Hawkins, Deborah
APPLICANT: Davies, Huw Maelor

```

Db      1528  GCGTGCATGCGACGTCAT  1545
          |||
RESULT  14
US-08-964-127-1
; Sequence 1, Application US/08964127
; Patent No. 6277505
; GENERAL INFORMATION:
; APPLICANT: Grandearl, Andrew David John
; TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE

```

;; TITLE OF INVENTION: MOLECULES
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: FastSeq for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/964,127
;; FILING DATE: 06-NOV-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Crews, Ph.D., L. Lee
;; REGISTRATION NUMBER: P-43,567
;; REFERENCE/DOCKET NUMBER: 07334/038001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2460 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: Genomic DNA
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 498....2057
US-08-964-127-1

Query Match 3.8%; Score 68; DB 4; Length 2460;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1726 aaaaaaaaaaaaaaaaaaagggcgccgctctagaggatccaaagcttacgtacgcg 1785
|||||
Db 2393 AAAAAAAAAAAAAAAAAAAGGGCGCGCTCTAGAGGATCCAAAGCTTACGTACGCG 2452
QY 1786 tgcatgcg 1793
Db 2453 TGCATCGG 2460

RESULT 15
US-09-118-442-31
;; Sequence 31, Application US/09118442B
;; Patent No. 6197561
;; GENERAL INFORMATION:
;; APPLICANT: Martino-Catt, Susan J.
;; APPLICANT: Wang, Hongyu
;; APPLICANT: Beach, Larry R.
;; APPLICANT: Wang, Xun
;; APPLICANT: Bowen, Benjamin A.
;; TITLE OF INVENTION: Genes Controlling Phytate Metabolism in
;; TITLE OF INVENTION: Plants and Uses Thereof
;; FILE REFERENCE: 0706
;; CURRENT APPLICATION NUMBER: US/09/118,442B
;; CURRENT FILING DATE: 1998-07-17
;; EARLIER APPLICATION NUMBER: 60/055,446
;; EARLIER FILING DATE: 1997-08-11
;; EARLIER APPLICATION NUMBER: 60/055,526
;; EARLIER FILING DATE: 1997-08-08

;; EARLIER APPLICATION NUMBER: 60/053,944
;; EARLIER FILING DATE: 1997-07-28
;; NUMBER OF SEQ ID NOS: 31
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 31
;; LENGTH: 1255
;; TYPE: DNA
;; ORGANISM: Zea mays
US-09-118-442-31

Query Match 3.7%; Score 67; DB 4; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 aaaaaaaaaaaaaaaaaaagggcgccgctctagaggatccaaagcttacgtacgcg 1793
|||||
Db 1161 aaaaaaaaaaaaaaaaaaagggcgccgctctagaggatccaaagcttacgtacgcg 1220
QY 1794 acgtcat 1800
|||||
Db 1221 acgtcat 1227
Search completed: March 8, 2002, 23:42:50
Job time: 1412 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 23:14:58 : Search time 1204.3 Seconds
(without alignments)
16061.116 Million cell updates/sec

Title: US-09-645-337-3

Perfect score: 1800

Sequence: 1 gtgccacacactcctagtaa.....acgcgtgcagtcgaagctcat 1800

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 537289281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estfun:
2: em_esthum:
3: em_estin:
4: em_estom:
5: em_estpl:
6: em_estba:
7: em_estro:
8: em_estov:
9: em_hic:
10: gb_est1:
11: gb_est2:
12: gb_hic:
13: gb_gss:
14: em_gss_fun:
15: em_gss_hum:
16: em_gss_inv:
17: em_gss_pln:
18: em_gss_pro:
19: em_gss_rnd:
20: em_gss_vrt:
21: em_gss_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	608	33.8	609	10	AV560183	AV560183
2	509.2	28.3	553	10	AI994522	AI994522 701498504
3	428.8	23.8	737	11	BI177518	BI177518 ESTS18463
c 4	380.8	21.2	385	10	AV567115	AV567115
5	365	20.3	765	10	AJ394397	AJ394397
6	353	19.6	999	10	AL518877	AL518877
7	347.2	19.3	977	13	CNS072YS	AL426842 clone BA0
c 8	347	19.3	907	13	CNS06FTS	AL414998 T3 end of
9	343.4	19.1	609	10	AI726977	AI726977 BNGCH1702
c 10	342.2	19.0	1030	13	CNS06MLI	AL405628 T3 end of
11	341	18.9	617	11	BF324960	BF324960 su29e12.y
12	340.2	18.9	919	10	AL531607	AL531607

13	334.2	18.6	621	10	AW217600	AW217600
14	333.6	18.5	431	10	AA394745	AA394745
15	332.2	18.5	847	10	AL558916	AL558916
16	329.6	18.3	946	10	BE036122	BE036122
17	325.8	18.1	640	11	BG449764	BG449764
18	322.6	17.9	577	11	BF176911	BF176911
19	321	17.8	910	11	BG756668	BG756668
20	319.4	17.7	719	10	AU132519	AU132519
c 21	318.8	17.7	881	13	CNS074AN	AL428565 clone BA0
22	318.8	17.7	898	10	AL541430	AL541430
23	317.2	17.6	917	11	BI118849	BI118849
24	316.8	17.6	819	10	BE558877	BE558877
25	309.8	17.2	986	10	AL536160	AL536160
26	309.6	17.2	597	10	AW308961	AW308961
27	308.4	17.1	998	10	AL555361	AL555361
28	305	16.9	910	10	AL546378	AL546378
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32	294.6	16.4	806	11	BG755703	BG755703
c 33	290.6	16.1	1107	13	CNS07B7W	AL437538 T7 end of
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37	286	15.9	687	10	AU138897	AU138897
38	285.8	15.9	605	11	BI097160	BI097160
39	285.8	15.9	631	10	BE325992	BE325992
40	285.6	15.9	709	11	BG027036	BG027036
41	285.2	15.8	834	10	BE742797	BE742797
42	285.2	15.8	947	11	BG366766	BG366766
c 43	284.6	15.8	1078	13	CNS077A8	AL432438 T3 end of
44	283.8	15.8	1005	10	AL523091	AL523091
45	283.6	15.8	577	10	AW398856	AW398856

ALIGNMENTS

RESULT 1
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LOCUS AV560183 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ13011F 3', mRNA sequence.
ACCESSION AV560183
VERSION AV560183.1 GI:8731609
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 609)
AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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QY 1081 gccgttggtggttatgagactgcagttgctgttggtgagtagagccgacacaaactc 1140
Db 609 GCCGTTGCTGTTGTTATGAGACTGCAGTTGCTGTTGGAGTAGAGCGGACAACTC 550

QY 1141 cttacaatgagattattgagattattcgccagattatacaacttcattgacccaagt 1200
Db 549 CCTTAAATGAGTATTGAGTATTTCGCCAGATTATACGCTTATGTCGACCAAGT 490

QY 1201 cctatgagaatttaaacacgcccacaaagatatggagagataagaacacgttgcgaa 1260
Db 489 CCTATGGAGAATTTAAACACGCCCAAGATATGGAGAGGATAGGAACACGTTGCTGGA 430

QY 1261 caacttcgggactaatacacgcactagctccagtttccagcacacacaccacgtcaat 1320
Db 429 CAACCTTCGGGACTAATACACGCACCTAGCTGCCAGTTTCAGCACACACACCACTCAAT 370

QY 1321 cgagtttggacgagccggaagatgacatggagagacacaaacccctgcgaatnaggat 1380
Db 369 CGAGTTTTCGACGAGCCGGAAGATGACATGGAGACAAACCAACCTCGCATCTGGAGT 310

QY 1381 ggaactgcgaactatgaatcacagacgagtgatgataaaactcttcattgattactca 1440
Db 309 GGAACCTGCACATTAATGATCAACAGATGACGATGATGATAAACCTCTTCATGGTTACTCA 250

QY 1441 tgcgtggtggcgcaactacgacgaggaactctaccggtgaagatgaatgagatgacat 1500
Db 249 TGTGCTGTGGCGCAACTACGACAGGACTCTACCGGTGAAGATGAATGATGACCAT 190

QY 1501 aaccagagcagacgagtaactcctccatctgcttaaacacagcttgatggtgtctc 1560
Db 189 AACCAGAGCCAGACGTAATCCTCCATCGTCTTAAACACAGCTTGATGTTGTGTCTC 130

QY 1561 ttttgccatataatgtcgcagatttaagaacaaagttaggggaatgaatgattctt 1620
Db 129 TTTTGCCATATGATTAATGTGCGCAGATTTAAGAACAGATTAGGGGAATGAATGATCTT 70

QY 1621 tgatgttttccagcaaccttttgagttctgtgaaacgcgtgcatgtattagaaacagtg 1680
Db 69 TGATGTTTTTTCAGCAACCTTTTGAGTTCTGTGAAAACGCTGCATTGATTAGAACAGTGA 10

QY 1681 caactgact 1689
Db 9 CAACGTGACT 1

RESULT 2
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LOCUS
DEFINITION 701498504 A. thaliana, Ohio State clone set Arabidopsis thaliana
ACCESSION A1994522
VERSION A1994522.1 GI:5841427
KEYWORDS EST.
SOURCE
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 (bases 1 to 553)
AUTHORS Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, P.,
Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T.,
Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobrigha, A., Murty, L.,
Turner, C., Krikorian, S., Elder, L. and Hanson, D.

TITLE Arabidopsis thaliana Gene Expression MicroArray
JOURNAL Unpublished (1999)
COMMENT Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.
FEATURES
Location/Qualifiers
source 1..553
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/db_xref="taxon:3702"
/clone="701498504"
/clone.lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the
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BASE COUNT 125 a 129 c 141 g 158 t
ORIGIN

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Matches 540; Conservative 0; Mismatches 13; Indels 3; Gaps 2;

QY 313 cgcctagcctcgctgacgctccgatatcgccgattccattccgcccggagtagttgac 372
Db 1 CGCCCTAGCCTCGCTGAGCCCTCCGATATCGCCGCGATTCATTCCGCCGAGTATGTTGAC 60

QY 373 ttcctgcttccttgcgcggaatctatggcgcatccttcgctgcacaaacctaaag 432
Db 61 TTCCTCGCTTCCTGTCGCCGAATCTATGGCGATCCTTCGCTGCAGCAACCTAAGG 120

QY 433 cgattcaatgctcgagagattgctgcttccttcgacgagacttttgattttgacctgct 492
Db 121 CGATTCAATGTCGGTGAGGATTGCTGCTTCGACGGACTTTTGTGATTTTTCGCGTCT 180

QY 493 tccgcggaggttctattggtgctgcgctcaaatataacacagagcgctgatatcgt 552
Db 181 TCCGCCGAGGTTCTATTGGTGTGCTGCCGTCAATTAACACAGACGAGCTGATATCGCT 240

QY 553 atcaattggcggtggttccaccatgcttaagaagaagcgaggtcttggttttgcatt 612
Db 241 ATCAATTGGGGCTGTGGGCTTCACCATGCTAAGAAAAGCGAGGCTTCTGGGTTTGTCTAT 300

QY 613 gtaaacacatcgctagagattctgagttgctcaagattttaaagcggttctctac 672
Db 301 GTAAACACATCGTGTCTAGGATTCTGGAGTTGCTCAAGATGTTTAAAGCGGTTCTCTAC 360

QY 673 atagattatgattccaccatggagatggagtggaagaagcggttttacaccactgata 732
Db 361 ATAGATTATGATGCCACCATGGAGATGGAGTGGAGAGAGCGTTTACACACCTGATAGA 420

QY 733 gttatgacttttttccacaaatttggggaacttttccacaggaactggtccacataaga 792
Db 421 GTTATGACTGTTTCTTTTCCAAATTTTGGGG--CTCTTTCCAGGAACCTGTCACATAAGA 478

QY 793 gatgttgctgtaaaaggaatactatgctctaaatgttccactaaacagatggtatg 852
Db 479 CATGTTCCGCTGAAAAGGGAATACTACTGCTCTTAATG--TCCACTAAACGATGGTATG 537

QY 853 gacgatgaaagtctcc 868
Db 538 GACGATGAAAGTTCCTCC 553

RESULT 3
B1177518
LOCUS
DEFINITION B1177518 737 bp mRNA EST 09-JUL-2001
B1177518 EST518463 CSTE Solanum tuberosum cDNA clone cSTE10D9 5' sequence,
B1177518 mRNA sequence.
ACCESSION B1177518
VERSION B1177518.1 GI:14643329
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QY	1351	gagacaacaccaaacctcgcabnttgtagtggaaactgcgaccttatgaatacacagagtgc	1410 	Dd	325	GAGACAACCAAACCTCCCATCTGGAGTGGAATCGGACTTATTGAATCAGACAGTGAC	266 		
QY	1411	gatgatataaacctcttcattcggttgtactcatgctgtagtggcgcaactacgcagcagac	1470 	Dd	265	GATGATATAAACCTTCCTCATGGTGTACTCATCTCGTGGTGGCGAATACGACAGGGAC	206 		
Qy	1471	tctaccggtgaagatgaaatgatgacataaaccccagcgcacagacgtgaatcctccccatcg	1530 	Dd	205	TCTACCGGTGAAGATGAAATGSATGACGATAACCCAGCAGCAGACGTGAATCTCTCCATCG	146 		
Qy	1531	tctaaccacagcttgatggttggtgtctctcttttgcctatatgaatgtgcgcagattta	1590 	Dd	145	TCTTAACCAAGCTTGATGGTGTGGTGTCTCTTTGCCATATGATAATGTGGCGAGATTTA	86 		
Qy	1591	agaacaagttaggggaatgaatgatctcttgatgcttttttacgcaaccttttgagttct	1650 	Dd	85	AGAAACAAGTTTAGGGGAATGAATGATCTTTGATGTTTTTTCAGCAACCTTTTGAGTTCT	26 		
Qy	1651	qtgaacacgcgtgattgattagaac	1675 	Dd	25	GTGAACCGATGCATTGATTAGAAC	1 		
RESULT 5									
AJ394397									
LOCUS	AJ394397	765 bp	mRNA	EST	25-JAN-2001				
DEFINITION	AJ394397	dkfz426	Gallus gallus cDNA clone 19d16r1,	mRNA sequence.					
ACCESSION	AJ394397								
VERSION	AJ394397.1	GI:7124259							
KEYWORDS	EST.								
SOURCE	chicken.								
ORGANISM	Gallus gallus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;								
AUTHORS	Phasianinae; Gallus. 1 (bases 1 to 765) Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy, J., Korn,B. and Buerstedde,J.M.								
TITLE	A large database of chickenursal ESTS as a resource for the analysis of vertebrate gene function								
JOURNAL	Genome Res. 10 (12), 2062-2069 (2000)								
MEDLINE	20568495								
COMMENT	Contact: Buerstedde JM Cellular Immunology Heinrich-Pette-Institute Martinistr. 52, 20251 Hamburg, Germany Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html. Location/Qualifiers 1..765 /organism="Gallus gallus" /strain="CB" /db_xref="taxon:9031" /clone="19d16r1" /clone_lib="dkfz426" /tissue_type="Bursa of Fabricius"								
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Q	y		494	ccgcggagggttctatggtcgcqtcgaattaaacagacagagacgctataatcgcta	553
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Q	y		554	tcaattgggcggttggtctcacactgaacaaaacgaggtctctgggttttgtcatg	613
D	b		125	TTAATGGCTGGAGAGACTTCACCATGCCAAGAAGTCAGAGGCATCTGGTTTTTTTTTATG	184
Q	y		614	taaacgacatcgtcgtagggtctcgaagtctcgaagtctcgaagtcttaagcgggtctctaca	673
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D	b		305	TCATGACAGTATCATTTCCATAGATAGTGTGAATATTTTCCAGGCACAGGGGACCTTAGG	364
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Q	y		914	agccagaggcagtggttcttcagtggtggtgcgtcctctaaagtggtgagtcggtggtt	973
D	b		485	AGCCAGTGTGTAGTATTACAGTGTGGAGCAGATTCAATGCTGTGTTAGTGTGGGAT	544
Q	y		974	gcttcaacttatcagtcgaagggtcacogctgattgcttcggtctcttaagatcttacaacg	1033
D	b		545	GCTTTAATCTTACTGTTTAAAGGTCATGCAAAATGTGTGGAAGTTGTTAAAGACCTTCACT	604
Q	y		1034	tctctcagtggttggttggtgaagggtatactattcgaaatggtgccggttggtcgtt	1093
D	b		605	TGCCATTGCTGATGTTAGGAGAGGTGGATATATTTCGCAATGTTTGCATGATGCTGGA	664
Q	y		1094	gttatgagactcagtgctgtctgttgaglagagccgcgacacaaactcccccttacaatg	1153
D	b		665	CATATGAACCTGCTGTGCTTGTAGATTGGGAAATTCCTAATGAATTACCATACCTGATT	724
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DEFINITION			AL518877 LTI_NFL011_NBC1 Homo sapiens cDNA clone CSDAO11VGL15 prime, mRNA sequence.		
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VERSION			AL518877.1		
KEYWORDS			GI:12782370		
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ORGANISM			human.		
REFERENCE			Homo sapiens		
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomom		
TITLE			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL			1 (bases 1 to 999)		
COMMENT			Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
			Full-length cDNA libraries and normalization		
			Unpublished (2001)		
			Contact: Genoscope		
			Genoscope . Centre National de Sequencage		
			BP 191 J91006 EVRY cedex - France		
			Email: seqreg@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
			Location/Qualifiers		
FEATURES			1..999		
source			1..999		

/organism="Homo sapiens"
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 /clone="CS0DA011YG11"
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 /sex="male"
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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT	257 a	223 c	275 g	234 t	10 others
ORIGIN					

Query Match	19.6%	Score 353;	DB 10;	Length 999;
Best Local Similarity	62.6%	Pred. No. 2.1e-54;		
Matches	592;	Conservative	5;	Mismatches 340; Indels 8; Gaps 3;
QY	174	gcggcgagtcagtttaactctacagccgacgacatcgagactactactactacggtcaagcca	233	
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QY	234	cccgatgaagcctcacgcggtccgtatggctcagctagcttaactcaactcaacctcca	293	
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QY	294	ccgtcgcttagaatacagtcgcccagctcctgcgtgacgcctccgatatcgccgattcca	353	
Db	167	CCGAAAAATGGAAATCTATGCCCTCAAAAGCCAAATGCTGAGGAGATGACCAAGTACCA	226	
QY	354	ttcgccgagtatgtgaacttcctgcgtccgcttcggttcgcccgaatctatggcgatccttc	413	
Db	227	CAGCGATGACTACATTAATTTCTTGGCGCTCCATCCGTCACAGATAACATGTCGGAGTACAG	286	
QY	414	cgctgcacgaacacaaagcgattcaatgtcggtyagagattgctcgtcttcgcgcgact	473	
Db	287	C-----AAGCAGATGCAGAGATTCACGTTGGTGAGGACTGTCGAGTATTCGATGGCCT	340	
QY	474	tttggattttgcccgtcttcgcgcgaggttctattggtgctccgtccaaatataacag	533	
Db	341	GTTTGAGTCTCTCAGTTGTCTACTGGTGGTCTCTGTGCAAGTCTGTGAAACTTAATAA	400	
QY	534	acaggacgcgtgatcgtatcaattggggcgggtgggcttcacatgctaagaaaaagcca	593	
Db	401	GCACGACGCGACATCGCTGTAATTTGGCTGGGGGCTGCACCATCGAAAGAGTCGGA	460	
QY	594	ggctctgggttttgcgtatgtaaacgacatcgtgctagggaattctggagttgctcaagat	653	
Db	461	GGCATCTGGCTCTGTACGTCAATGAATCGTCTTGCCATCTCGNACTGCTTAAGTA	520	
QY	654	gtttaacggggtctctacatagatatgtatgtccacatggagatggagtggaagagc	713	
Db	521	TCACGAGAGGGTGTGTACATTGACATTGATATTCACCATGTCACGCGGTGGAAGAGGC	580	
QY	714	gttttacaccactgatagattatgaactgtttcttctccacaaattggggacttttccc	773	
Db	581	CTTCTACACCACGACCGGGTCATGACTGTGCTCTTCATAAAGTATGGAGAGTACTTCCC	640	
QY	774	aggaactggtcacataagagatgttgcgcgtcaaaaaagggaataactatgctcaaatgt	833	
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QY	834	tccactaaacgatggtatggacgatgaagtttccgcagctgttttagaccttattcca	893	
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Qy	954	aagt-ggtgatcgttggttggttcaacttatcagtcacaggtcagcgtatgtgccttc	1012
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LOCUS		977 bp	DNA
DEFINITION		clone BA0AB015009 of library BA0AB from strain CLIB 210 of	GSS
		Kluyveromyces lactis, genomic survey sequence.	
ACCESSION		AL426842	
VERSION		AL426842.1	GI:12210036
KEYWORDS		GSS.	
SOURCE			
ORGANISM		Kluyveromyces lactis.	
		Kluyveromyces lactis	
REFERENCE			
AUTHORS		Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
		Saccharomycetales; Saccharomycetaceae; Kluyveromyces.	
		1 (bases 1 to 977)	
		Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,	
		Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,	
		Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.	
		Genomic exploration of the hemiascomycetous yeasts: 11.	
TITLE		Kluyveromyces lactis	
JOURNAL		FEBS Lett. 487 (1), 66-70 (2000)	
MEDLINE		20584721	
REFERENCE			
AUTHORS		2 (bases 1 to 977)	
		Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,	
		Bolotin-Fukuhara,M., Bon,E., Broutier,P., Casaregola,S.,	
		de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,	
		Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,	
		Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,	
		Wincker,P. and Weissenbach,J.	
		Genomic exploration of the hemiascomycetous yeasts: 1. A set of	
		yeast species for molecular evolution studies	
TITLE		FEBS Lett. 487 (1), 3-12 (2000)	
JOURNAL		20584711	
MEDLINE		3 (bases 1 to 977)	
REFERENCE			
AUTHORS		Genoscope.	
TITLE		Direct Submission	
JOURNAL		Submitted (08-SP-2000) Genoscope - Centre National de Sequencage,	
		2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT		This GSS is part of a random genomic sequencing program of thirteen	
		yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces	
		exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,	
		Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces	
		lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia	
		angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,	
		Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to	
		5 kb were prepared and both extremities were sequenced. See	
		keywords for description of this sequence and for the sequence of	
		the other extremity of this insert.	
FEATURES		Location/Qualifiers	
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of Saccharomyces kluyveri, genomic survey sequence.

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ACCESSION      AL405628
VERSION        AL405628.1 GI:12168630
SOURCE        GSS.
ORGANISM      Saccharomyces kluyveri.
               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
               Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE      1 (bases 1 to 1030)
AUTHORS        Neuvéglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
               Gaillardin,C. and Casaregola,S.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 9.
JOURNAL        FEBS Lett. 487 (1), 56-60 (2000)
MEDLINE        20584719
REFERENCE      2 (bases 1 to 1030)
AUTHORS        Souclet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
               Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
               de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
               Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
               Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
               Wincker,P. and Weissenbach,J.
TITLE          Genomic exploration of the hemiascomycetous yeasts: 1. A set of
               yeast species for molecular evolution studies
JOURNAL        FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE        20584711
REFERENCE      3 (bases 1 to 1030)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
               2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
               seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT        This GSS is part of a random genomic sequencing program of thirteen
               yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
               exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
               Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
               lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
               angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
               Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
               5 kb were prepared and both extremities were sequenced. See
               keywords for description of this sequence and for the sequence of
               the other extremity of this insert.
FEATURES       Location/Qualifiers
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               1 putative frameshift(s)"
               /evidence=not_experimental
BASE COUNT    309 a 247 c 182 g 290 t
ORIGIN

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Query Match      19.0% ; Score 342.2; DB 13; Length 1030;
Best Local Similarity 59.9% ; Pred. No. 1.8e-52;
Matches 592; Conservative 1; Mismatches 390; Indels 6; Gaps 1;

QY 172 aagcgcgagtcagttacttctacgagcgcgagcgcgagactactactacggtcaaggc 231
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Db 983 AAAAGAGAGTTCCTACTCTATCATGTCGGACGTTGGAACTACGCTTATGGTCTGGT 924

QY 232 caccgcgataaacctcaccgcgagtcgctatgctcagcctaatactcattcaccctc 291
    || || || || || || || || || || || || || || || || || || || || ||
Db 923 CACCCAATGAACACACATAGATAAGATGACCCATCTCTTAATATGAACCTACGGGTG 864

QY 292 caccgctcgttagaactcagtcgcctcagctcgcgctcgcgctcgcgctcgcgctc 351
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RESULT 11

BF324960

LOCUS

DEFINITION

su29e12.y1 Gm-cl068 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:

Gm-cl068-624 5' similar to TR:Q9ZTP8 Q9ZTP8 HISTONE DEACETYLASE. ;

mRNA sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

soybean.

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabaceae; Papilionoideae; Phaseoleae;

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Db	214	CAGCGATGACTACATTAATTAATTTTCGCCTCCATCCGTCCAGATAACATGTCGGAGTACAG	273
Qy	414	cgctgcacgaacctaaaggcagattcaatgtcggtaggagattctctgtcttttcgcaggaact	473
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Qy	474	ttttgatttttgcgcgtcttcgcgcggaggttctatgtgtcgcgcgcaataaaacag	533
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Qy	534	acaggacgcctgatatcgcctatcaatttgggcgggtgggcttcaccatgctaaagaaagcga	593
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Qy	714	gtttacaccactgataagattatgactgtttcttccacaaatttggggacttttccc	773
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